```
  1 GAT TTT TTG TGA TAT CTT CTT CGG GGG GGG GGG GAA CCT ATT GTA TAA ACG CCA ACC AAC CGG
 64 CCC TTT TTT GGG TAC CTG GCC ATT TTA CTT GGC CCA TTT TGG TAA AAT GTT CCT TTC CCT GCG
127 TTA ATC CCC CTG ATT CCT TGT GGG ATA ACC CGT ATT CCC CCC CTT AGA GTG AAT TTG AAA ACC
190 CTT TCG CCC GGA AGG GGA CCG ACC GAG CCC AGC GAT TCA TGG AGC GAG GAA AGC GGG AAG AGC
253 GCC CAA TAC CCA AGC CGC CTC TCG CCG GCG CGT TGT GCG ATT CAT TAA TAC AGC TGC CAC GAC
316 AGG TTT CCC GAC TGG AAA GCG GTC AGT GAG CGC AAC ACA ATT AAT GTG AGT TAG CTC ACT CAT
379 TAG GCA CCC CAG GCT TTA CAC TTT ATG CTT CCG GCT CGT ATG TTG TGT GGA ATT GTG AGC GGA
442 TAA CAA TTT CAC ACA GGA AAC AGC TAT GAC CAT GAT TAC GTC CAA GCT CGA AAT TAA CCC TCA
505 CTA AAG GGA ACA AAA ACT GGA GCT CCA CCG CGG TGG CGG CCG CTC TAG AAC TAG TGG ATC CCC
568 CGG GCT CCA GGA ATT CGC CAC GAC CGG GAG GAC CGA GGA GGC GCC AGA CTA CGG GCG A   ATG
                                                                                   MET
629 GCG ACC CGC AGC CCT GGC GTC GTG ATT ATG GAT GAT TGG CCA GGG TAT GAC TTG AAT TTA TTC
    Ala Thr Arg Ser Pro Gly Val Val Ile MET Asp Asp Trp Pro Gly Tyr Asp Leu Asn Leu Phe
```

FIG. 1A

692 ACG TAC CCA CAG CAC TAT TAT GGA GAC TTG GAG TAT GTC CTC ATC CCT CAT GGT ATC ATT GTG
Thr Tyr Pro Gln His Tyr Tyr Gly Asp Leu Glu Tyr Val Leu Ile Pro His Gly Ile Ile Val

755 GAC AGA ATT GAG CGG CTG GCC AAG GAT ATT ATG AAA GAC ATA GGA TAT AGT GAC ATC ATG GTC
Asp Arg Ile Glu Arg Leu Ala Lys Asp Ile MET Lys Asp Ile Gly Tyr Ser Asp Ile MET Val

818 CTG TGT GTG CTT AAA GGG GGG TAC AAA TTC TGT GCT GAT CTC GTA GAA CAC CTT AAG AAC ATC
Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Cys Ala Asp Leu Val Glu His Leu Lys Asn Ile

881 AGC CGA AAT TCA GAT CGG TTT GTC TCA ATG AAG GTT GAT TTC ATC AGA CTA AAA AGT TAC AGG
Ser Arg Asn Ser Asp Arg Phe Val Ser MET Lys Val Asp Phe Ile Arg Leu Lys Ser Tyr Arg

944 AAT GAC CAG TCC ATG GGT GAG ATG CAG ATA ATC GGA GGC GGT GAT CTT TCA ACG CTG GCT GGA
Asn Asp Gln Ser MET Gly Glu MET Gln Ile Ile Gly Gly Gly Asp Leu Ser Thr Leu Ala Gly

1007 AAG AAT TTT CTC ATT GTT GAG GAT GTT GTC GGA ACT GGG AGG ACC ATG AAA GCA CTA CTC AGC
Lys Asn Phe Leu Ile Val Glu Asp Val Val Gly Thr Gly Arg Thr MET Lys Ala Leu Leu Ser

1070 AAT ATA GAG AAA TAC AAG CCC AAC ATG ATT AAG GTA GCC AGT TTG TTG GTG AAG AGA ACA TCC
Asn Ile Glu Lys Tyr Lys Pro Asn MET Ile Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser

1133 AGA AGT GAC GGC TTT AGA CCT GAC TAT GCT GGA TTT GAG ATT CCA CAC TTA TTT GTG GTG GGA
Arg Ser Asp Gly Phe Arg Pro Asp Tyr Ala Gly Phe Glu Ile Pro His Leu Phe Val Val Gly

FIG. 1B

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1196 TAT GCC TTA GAT TAC AAT GAA TAC TTC AGA GAT CTG AAT CAC ATA TGC GTC ATC AAT GAG CAC
Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile Asn Glu His

1259 GGG TAA AGG AAA ATA TCG AGT CTT AAA GAC ATG AAT TCT CAC CAC TAA AGG CCC CAG ATA GGA
Gly STP

1322 TCA TTT TTA CGC CTG TCT TGG GGA GCC AGT TGC AAG TTG GGC CCC CCC GGA TCT TCA TCA GGA

1385 GG

FIG. 1C

```
  1  MATRSPGVVISDDEPGYDLDLFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKE  56
     |||||||||| || |||||:||..|.|| :||| |:||||:|:||.||||:|:||:
  1  MATRSPGVVIMDDWPGYDLNLFTYPQHYYGDLEYVLIPHGIIVDRIERLAKDIMKD  56

 57  MGGHHIVALCVLKGGYKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSYCNDQSTG  112
     :|  .|:.|||||||||| |||::.:|.:.||||| :.|.||||||||| |||| |
 57  IGYSDIMVLCVLKGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSYRNDQSMG  112

113  DIKVIGGDDLSTLTGKNVLIVEDIIDTGKTMQTLLSLVRQYNPKMVKVASLLVKRT  168
     ::.:|||:|||||.|||.|||||:::||:||..||| : .|.|.|:||||||||||
113  EMQIIGGGDLSTLAGKNFLIVEDVVGTGRTMKALLSNIEKYKPNMIKVASLLVKRT  168

169  PRSVGYKPDFVGFEIPDKFVVGYALDYNEYFRDLNHVCVISETGKAKYKA        218
     .|| |::||:.|||||. ||||||||||.|||||||:|||.| |  |...
169  SRSDGFRPDYAGFEIPHLFVVGYALDYNEYFRDLNHICVINEHG*RKISS        218
```

FIG.2

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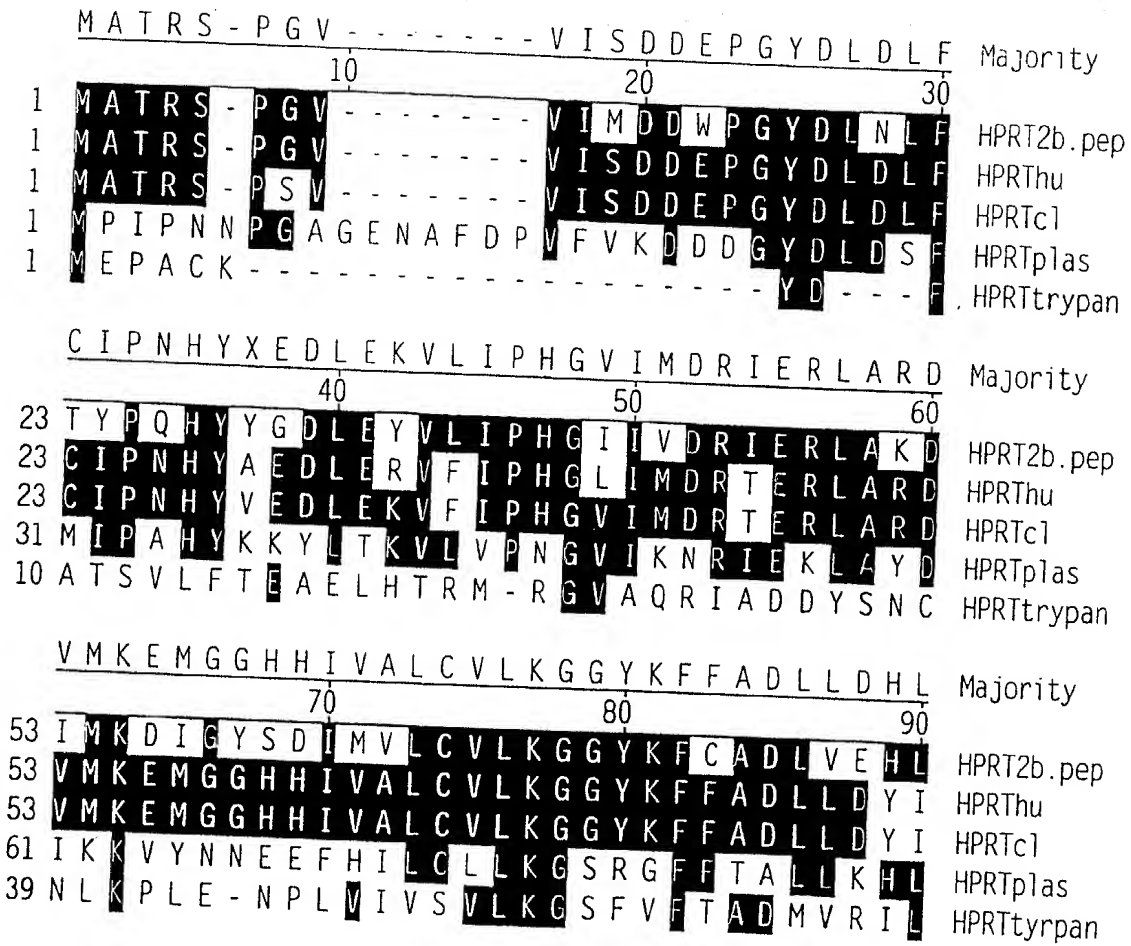

FIG.3A

09920705 "07T20T

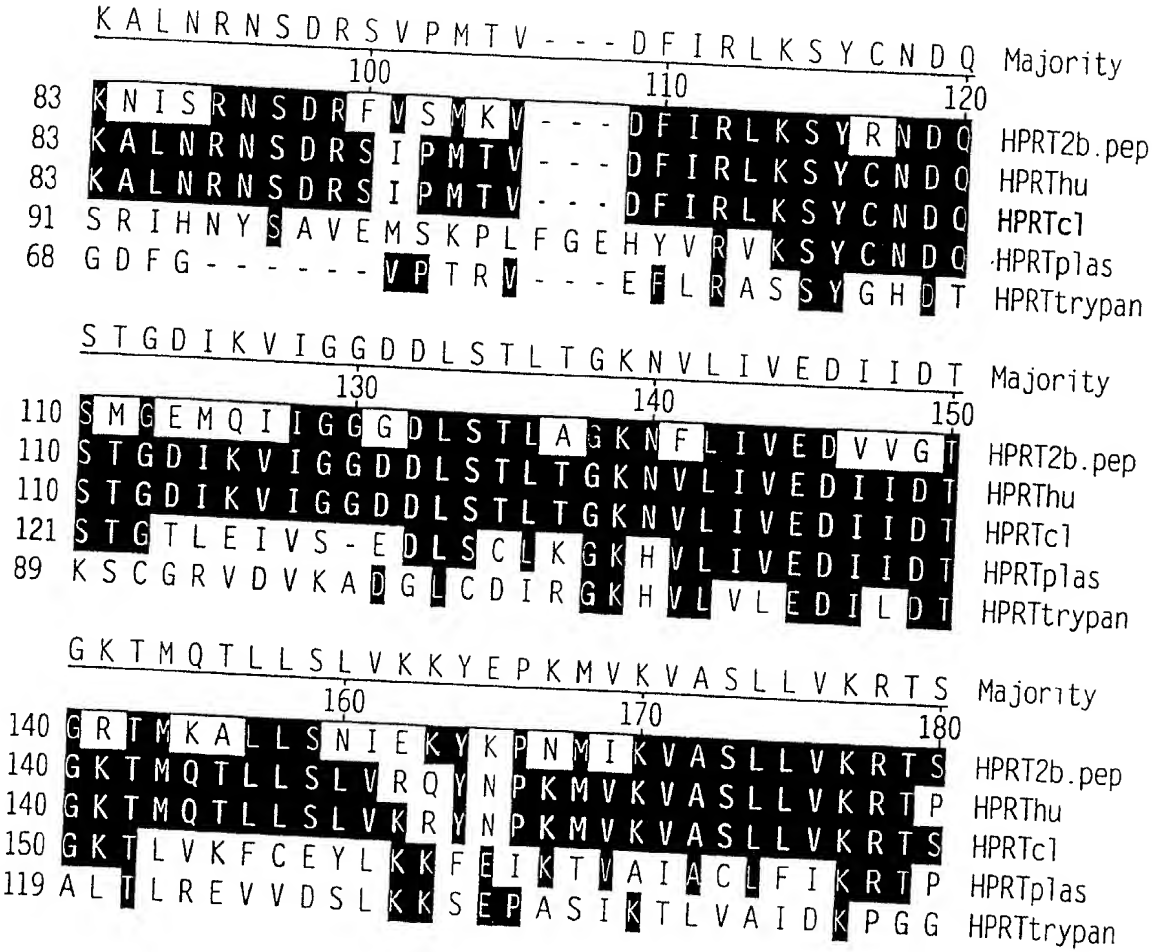

FIG.3B

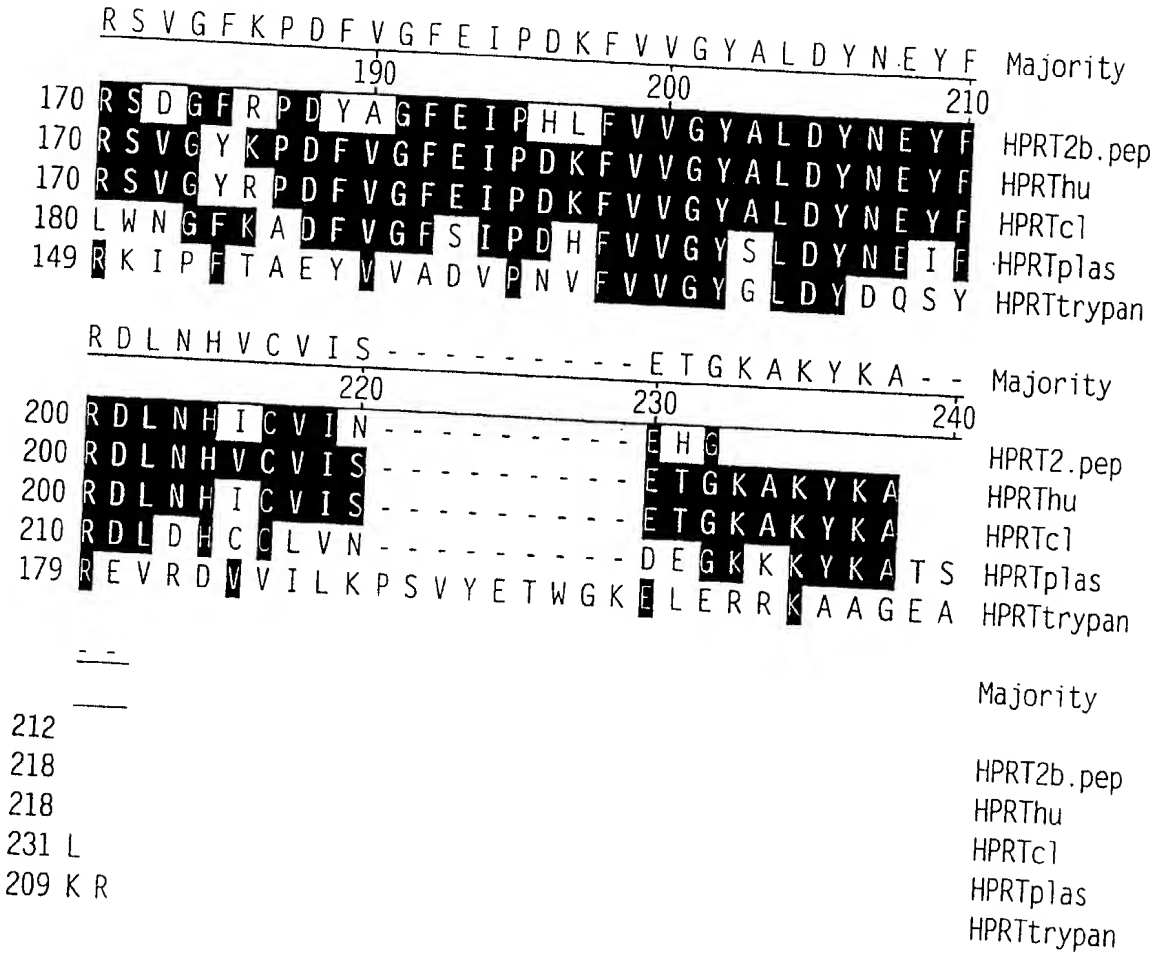
R S V G F K P D F V G F E I P D K F V V G Y A L D Y N E Y F Majority
190
200
210
170 R S D G F R P D Y A G F E I P H L F V V G Y A L D Y N E Y F
170 R S V G Y K P D F V G F E I P D K F V V G Y A L D Y N E Y F HPRT2b.pep
170 R S V G Y R P D F V G F E I P D K F V V G Y A L D Y N E Y F HPRThu
180 L W N G F K A D F V G F S I P D H F V V G Y S L D Y N E I F HPRTcl
149 R K I P F T A E Y V V A D V P N V F V V G Y G L D Y D Q S Y HPRTplas
HPRTtrypan
R D L N H V C V I S - - - - - - - - - E T G K A K Y K A - - Majority
220
230
240
200 R D L N H I C V I N - - - - - - - - - E H G
200 R D L N H V C V I S - - - - - - - - - E T G K A K Y K A HPRT2.pep
200 R D L N H I C V I S - - - - - - - - - E T G K A K Y K A HPRThu
210 R D L D H C C L V N - - - - - - - - - D E G K K Y K A HPRTcl
179 R E V R D V V I L K P S V Y E T W G K E L E R R K A A G E A T S HPRTplas
HPRTtrypan
- -
Majority
212
218 HPRT2b.pep
218 HPRThu
231 L HPRTcl
209 K R HPRTplas
HPRTtrypan

FIG.3C

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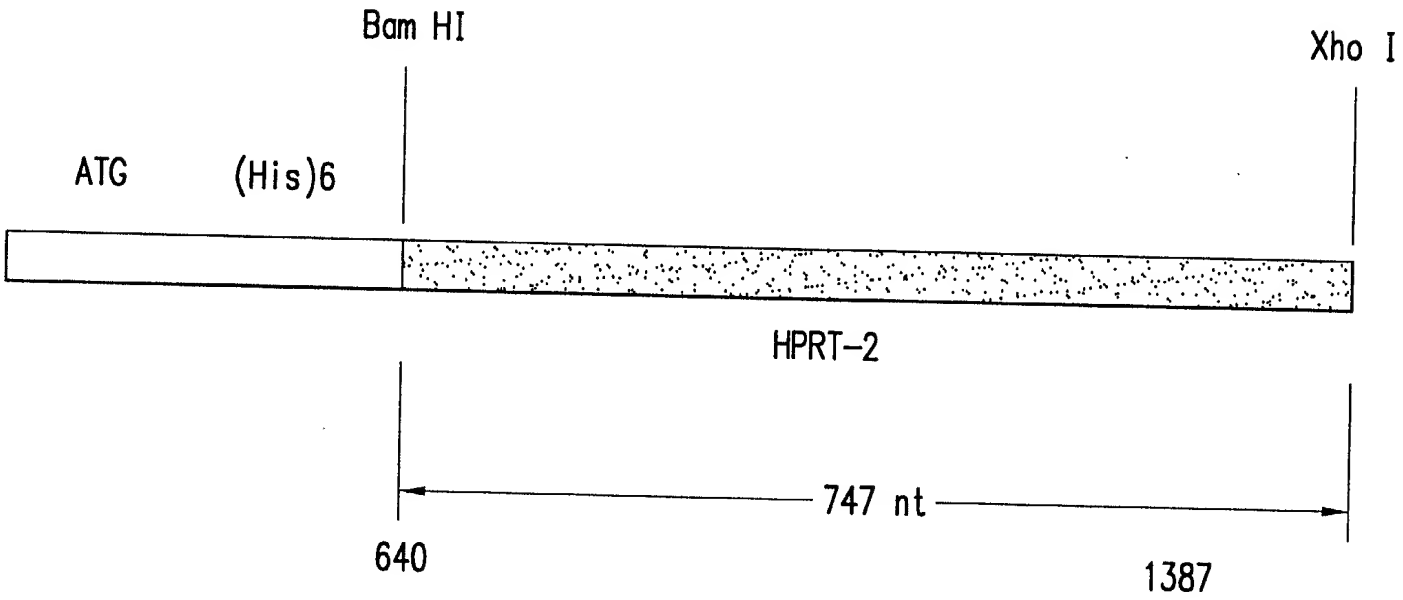

FIG.4

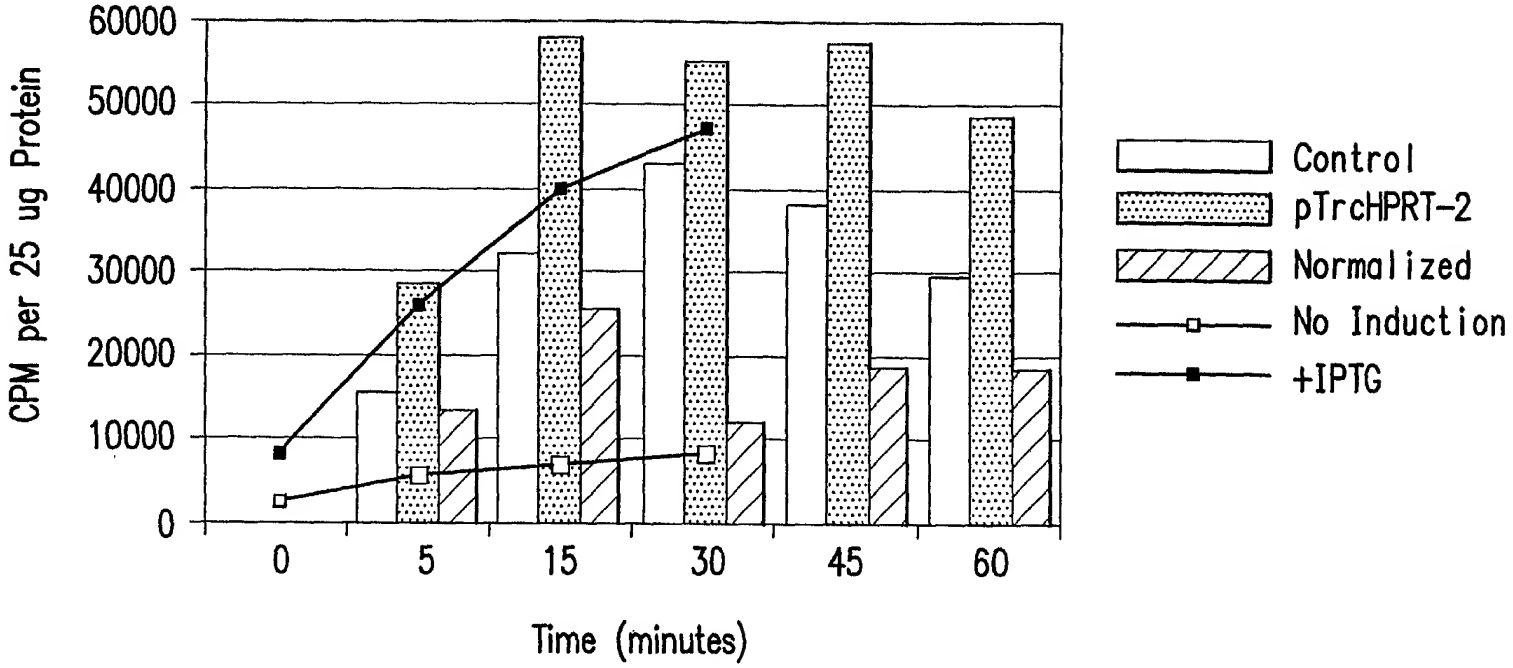
60000
50000
40000
30000
20000
10000
0
CPM per 25 ug Protein
0
5
15
30
45
60
Time (minutes)
Control
pTrcHPRT-2
Normalized
No Induction
+IPTG

FIG.5